

SEQUENCE LISTING

<110> Luo, Ying
Mancebo, Halena

<120> NOVEL SYK KINASE-ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS, AND METHODS OF USE

<130> A-68412-1/RMS/DHR

<140> US 10/088,960
<141> 2002-03-22

<150> US 09/404,967
<151> 1999-09-24

<150> PCT/US 00/26338
<151> 2000-09-25

<160> 12

<170> PatentIn version 3.1

<210> 1
<211> 3955
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1473) ..(1473)
<223> "n" at position 1473 can be any base.

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<210> 2
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<212> PRT
<213> Homo sapiens

<220>
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<222> (373)..(373)
<223> "Xaa" at position 373 can be any amino acid.

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Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu
35 40 45

Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln
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Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr
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Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly
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Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu
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Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala
115 120 125

Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu
130 135 140

Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp
145 150 155 160

Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn
165 170 175

Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu
180 185 190

Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp
195 200 205

Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu
210 215 220

Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val
225 230 235 240

Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn
245 250 255

Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp
260 265 270

Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu
275 280 285

Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu
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Ala Val Gly Val Leu Glu Gly Lys Phe Glu Asn Thr Glu Met Phe
305 310 315 320

Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys
325 330 335

Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu
340 345 350

Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro
355 360 365

Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly
370 375 380

Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr
385 390 395 400

Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg
405 410 415

Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg
420 425 430

Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu
435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val
450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala
485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile
500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro
515 520 525

Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu
530 535 540

Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu
545 550 555 560

Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr
565 570 575

Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg
580 585 590

Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr
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Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn
610 615 620

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660 665 670

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Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln
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740 745 750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His
755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu
770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr
785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala
805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg
820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln
835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr
850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr
865 870 875 880

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900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg
915 920 925

Arg Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu
930 935 940

Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu
945 950 955 960

Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu
965 970 975

Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr
980 985 990

Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe
995 1000 1005

Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His
 1010 1015 1020

Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu
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Gly Arg
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<223> "n" at position 1473 can be any base.
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